FIG. 1

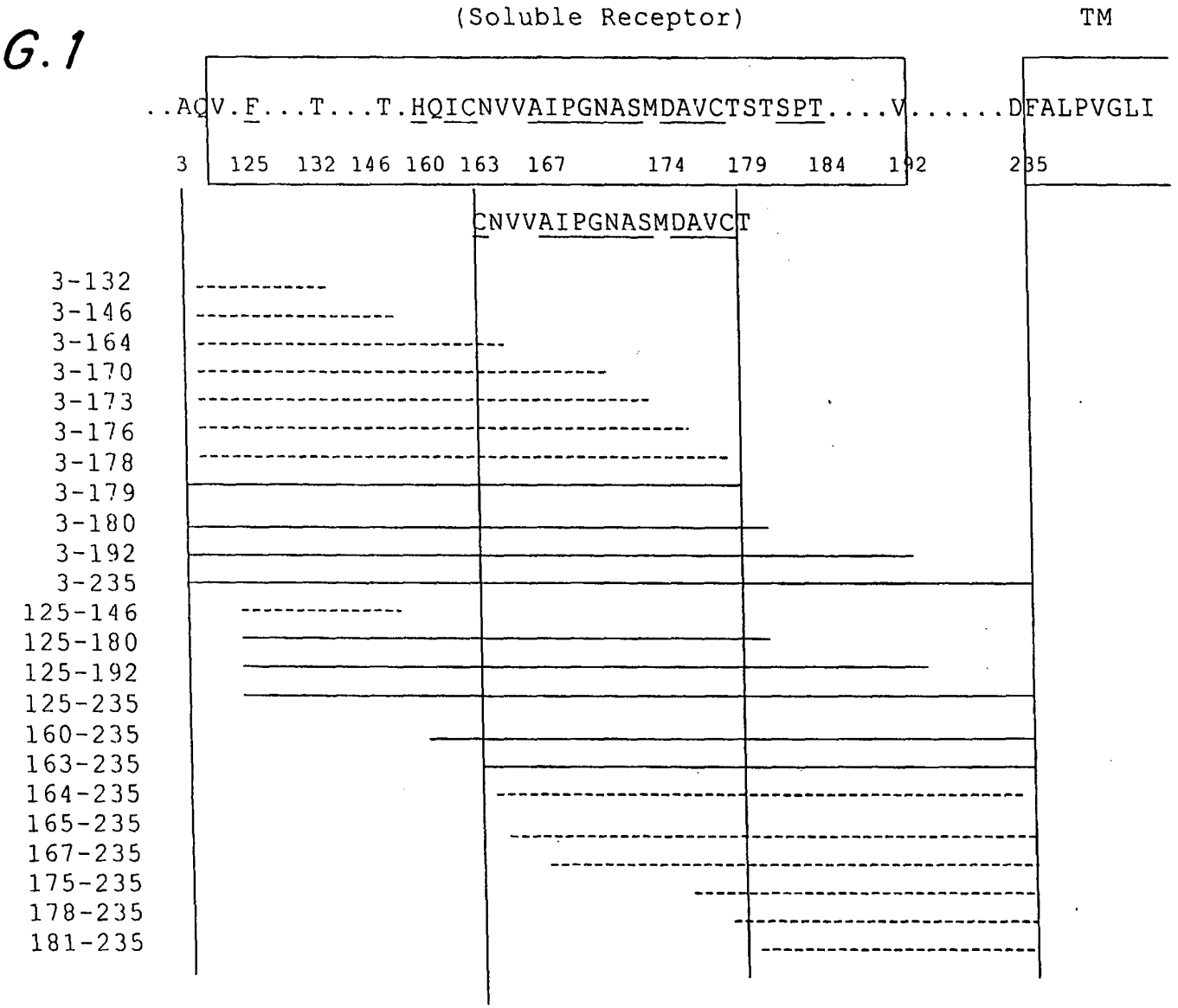

(Soluble Receptor)
TM
..AQV.F...T...T.HQICNVVAIPGNASMDAVCTSTSPT....V.....DFALPVGLI
3 125 132 146 160 163 167 174 179 184 192 235
CNVVAIPGNASMDAVCT
3-132
3-146
3-164
3-170
3-173
3-176
3-178
3-179
3-180
3-192
3-235
125-146
125-180
125-192
125-235
160-235
163-235
164-235
165-235
167-235
175-235
178-235
181-235

FIG. 2

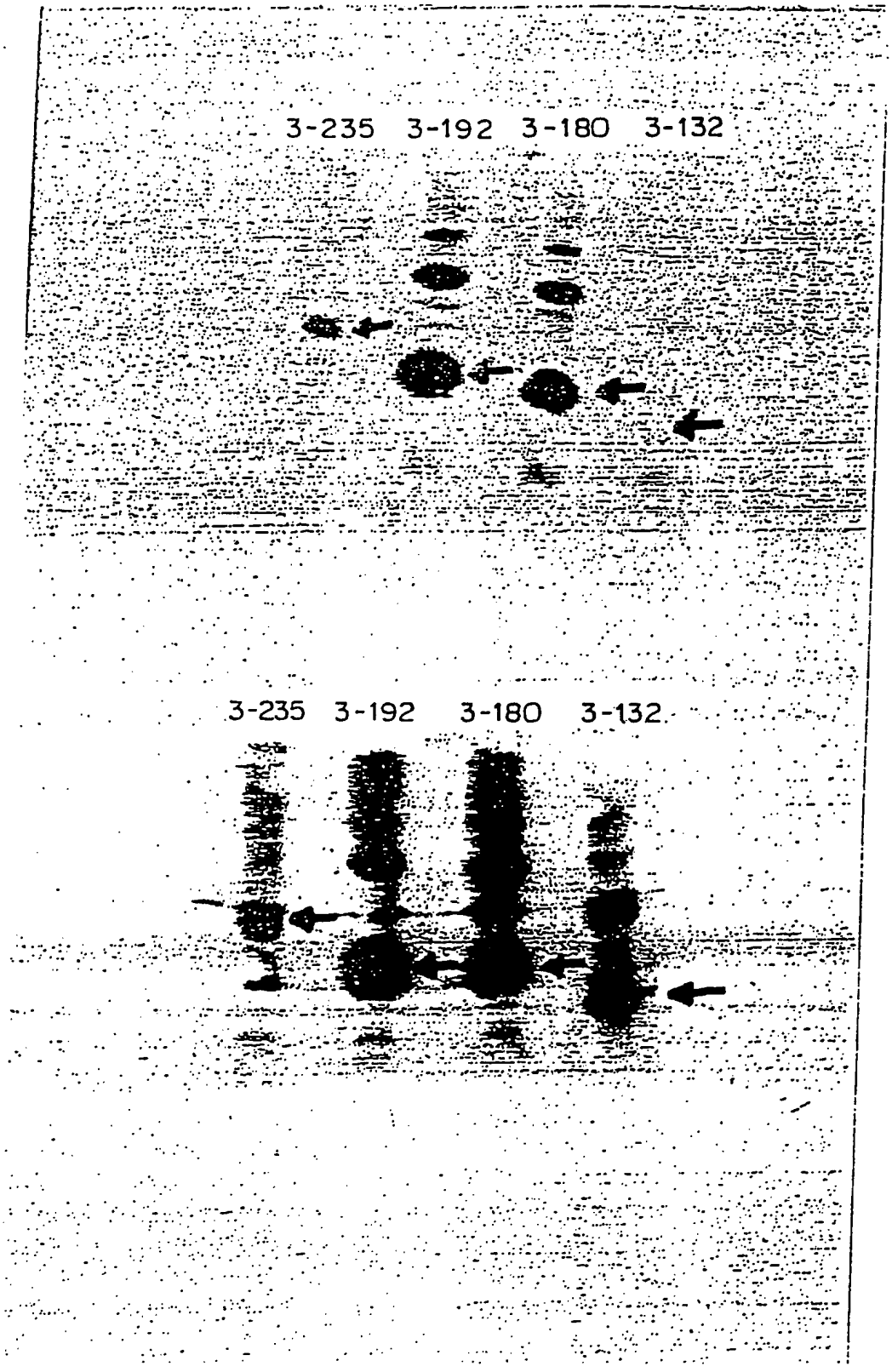


FIG. 3

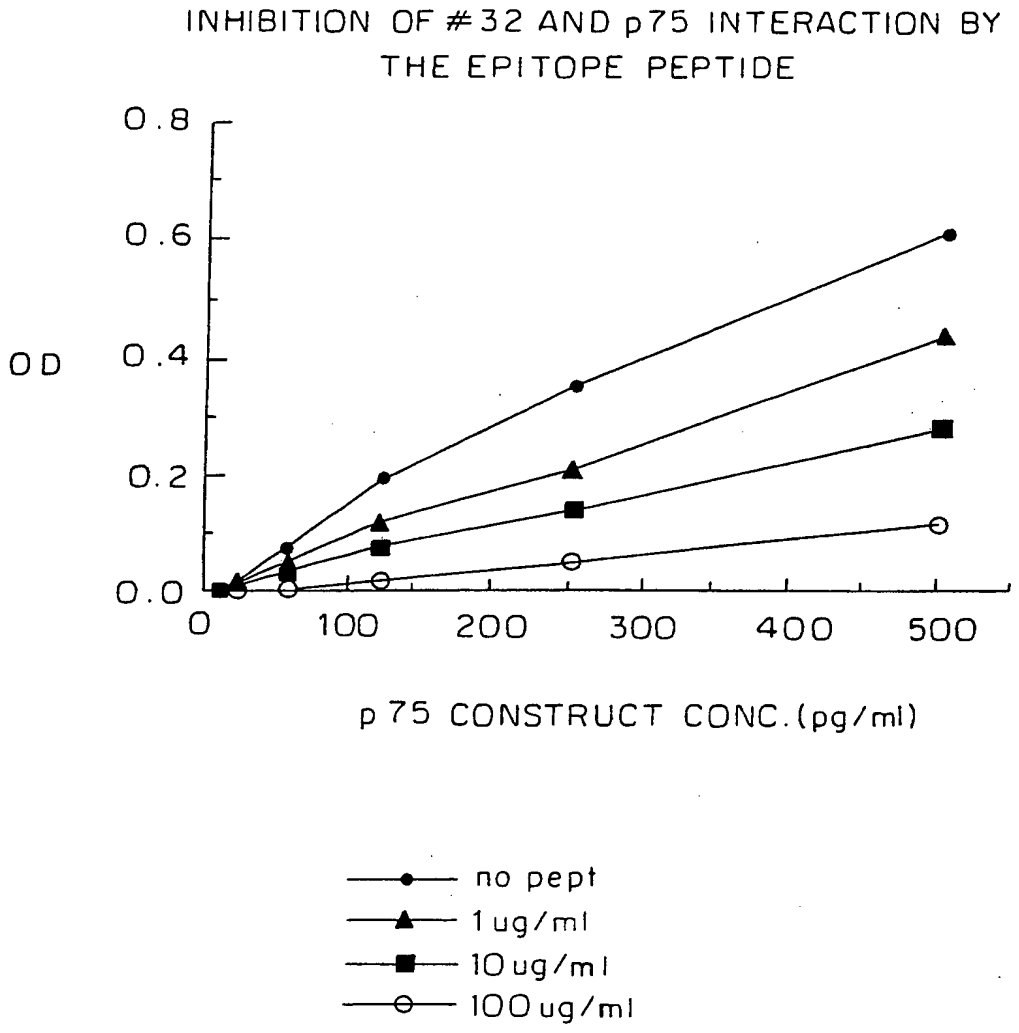

INHIBITION OF #32 AND p75 INTERACTION BY THE EPITOPE PEPTIDE
OD
0.8
0.6
0.4
0.2
0.0
0
100
200
300
400
500
p75 CONSTRUCT CONC.(pg/ml)
no pept
1 ug/ml
10 ug/ml
100 ug/ml

FIG. 4

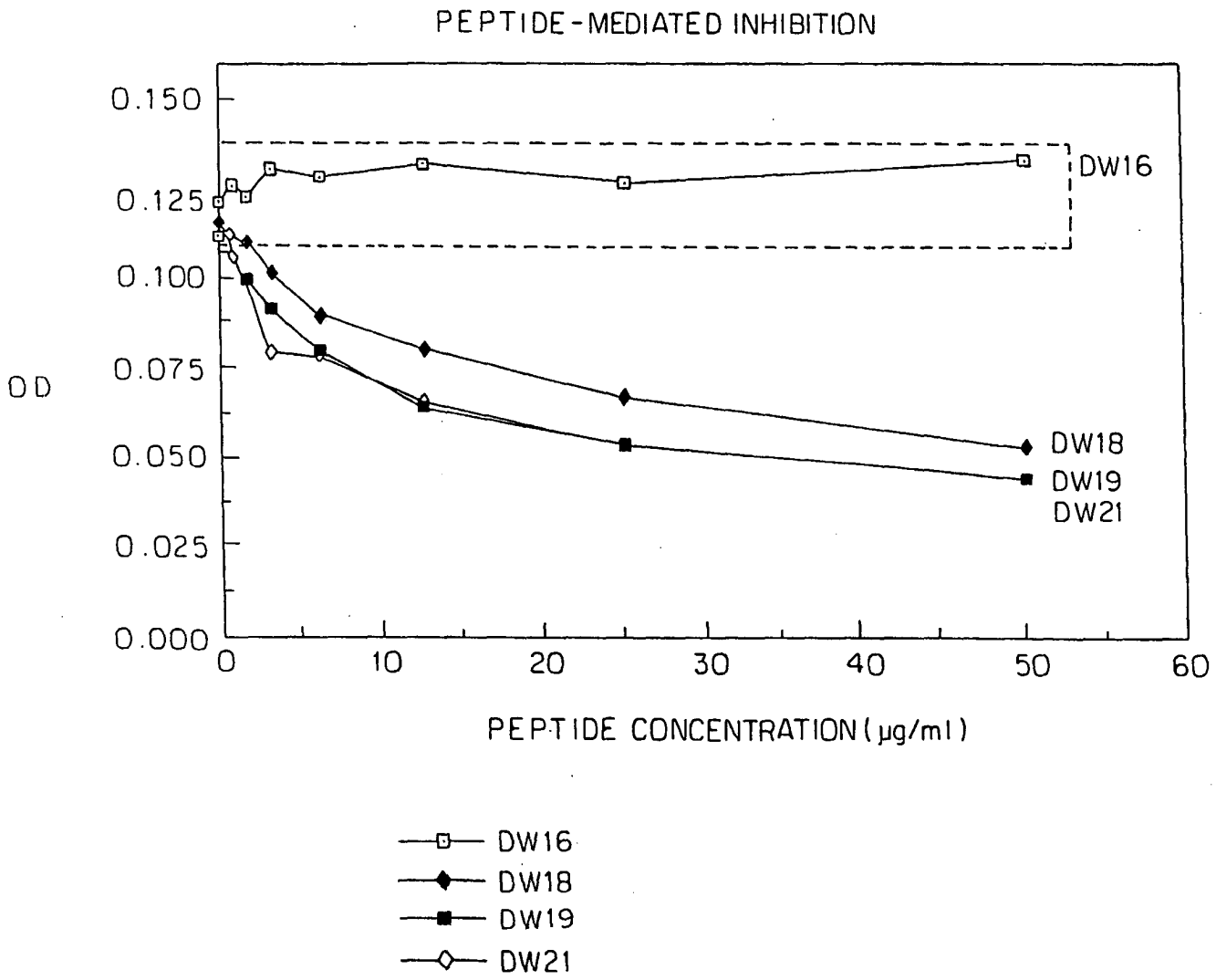

PEPTIDE-MEDIATED INHIBITION
OD
0.150
0.125
0.100
0.075
0.050
0.025
0.000
0
10
20
30
40
50
60
PEPTIDE CONCENTRATION (μg/ml)
DW16
DW18
DW19
DW21
DW16
DW18
DW19
DW21

FIG. 5A

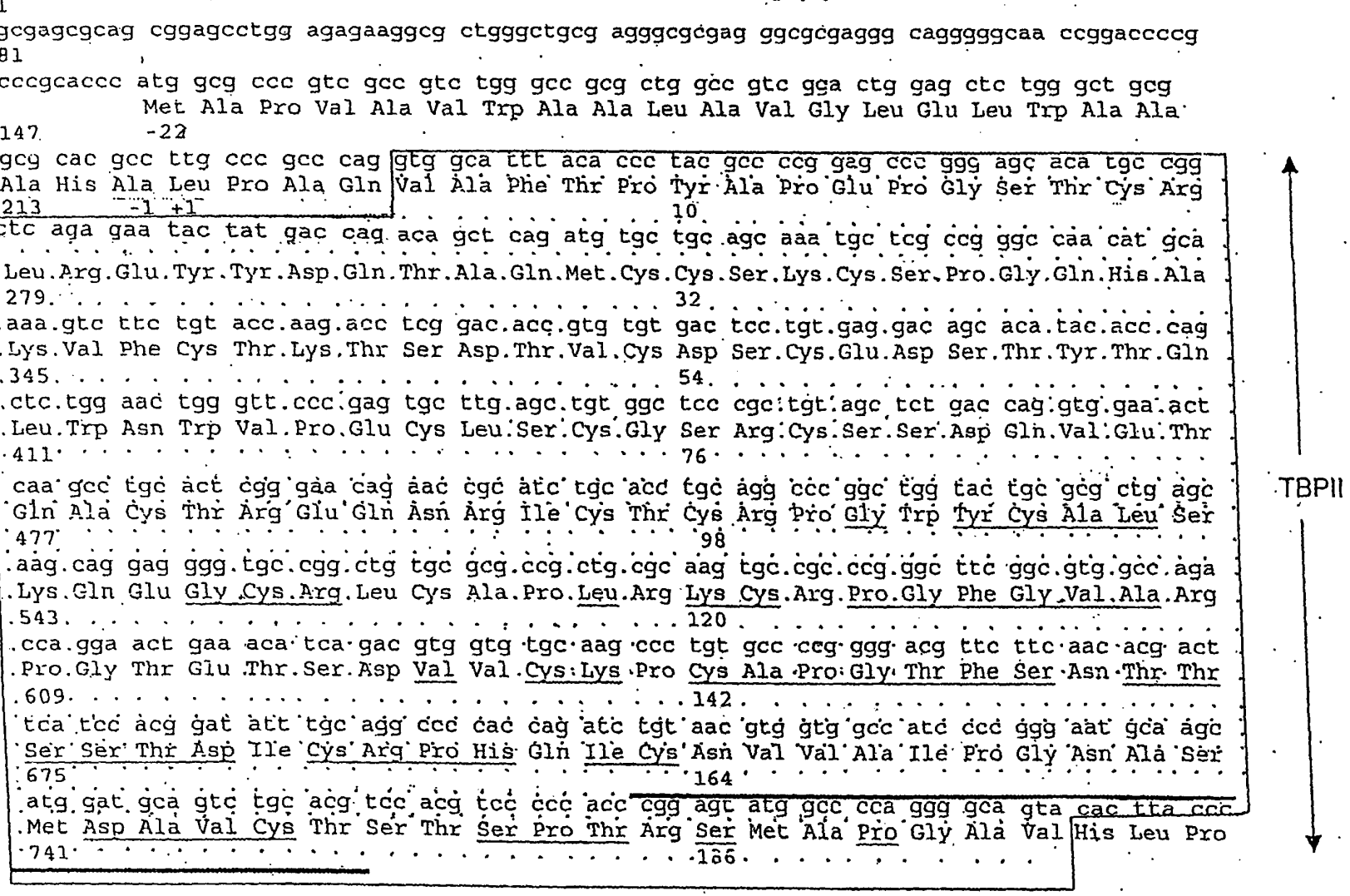

1
gcgagcgcag cggagcctgg agagaaggcg ctgggctgcg agggcgcgag ggcgcgaggg caggggcaa ccggaccccg
81
cccgcaccc atg gcg ccc gtc gcc gtc tgg gcc gcg ctg gcc gtc gga ctg gag ctc tgg gct gcg
Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala
147 -22
gcg cac gcc ttg ccc gcc cag gtg gca ttt aca ccc tac gcc ccg gag ccc ggg agc aca tgc cgg
Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg
213 -1 +1 10
ctc aga gaa tac tat gac cag aca gct cag atg tgc tgc agc aaa tgc tcg ccg ggc caa cat gca
Leu.Arg.Glu.Tyr.Tyr.Asp.Gln.Thr.Ala.Gln.Met.Cys.Cys.Ser.Lys.Cys.Ser.Pro.Gly.Gln.His.Ala
279 32
aaa gtc ttc tgt acc aag acc tcg gac acc gtg tgt gac tcc tgt gag gac agc aca tac acc cag
Lys.Val Phe Cys Thr.Lys.Thr Ser Asp.Thr.Val.Cys Asp Ser.Cys.Glu.Asp Ser.Thr.Tyr.Thr.Gln
345 54
ctc tgg aac tgg gtt ccc gag tgc ttg agc tgt ggc tcc cgc tgt agc tct gac cag gtg gaa act
Leu.Trp Asn Trp Val.Pro.Glu Cys Leu.Ser.Cys.Gly Ser Arg.Cys.Ser.Ser.Asp Gln.Val.Glu.Thr
411 76
caa gcc tgc act cgg gaa cag aac cgc atc tgc acc tgc agg ccc ggc tgg tac tgc gcg ctg agc
Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser
477 98
aag cag gag ggg tgc cgg ctg tgc gcg ccg ctg cgc aag tgc cgc ccg ggc ttc ggc gtg gcc aga
Lys.Gln Glu Gly Cys.Arg.Leu Cys Ala.Pro.Leu.Arg Lys Cys.Arg.Pro.Gly Phe Gly Val.Ala.Arg
543 120
cca gga act gaa aca tca gac gtg gtg tgc aag ccc tgt gcc ccg ggg acg ttc ttc aac acg act
Pro.Gly Thr Glu Thr.Ser.Asp Val Val.Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr
609 142
tca tcc acg gat att tgc agg ccc cac cag atc tgt aac gtg gtg gcc atc ccc ggg aat gca agc
Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser
675 164
atg gat gca gtc tgc acg tcc acg tcc ccc acc cgg agt atg gcc cca ggg gca gta cac tta ccc
Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val His Leu Pro
741 186
TBPII

FIG.5B

```
cag cca gtg tcc aca cga tcc caa cac acg cag cca act cca gaa ccc agc act gct cca agc acc
Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr
807                                                 208
tcc ttc ctg ctc cca atg ggc ccc agc ccc cca gct gaa ggg agc act ggc gac ttc gct ctt cca
Ser Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro
873                                                 230
gtt gga ctg att gtg ggt gtg aca gcc ttg ggt cta cta ata ata gga gtg gtg aac tgt gtc atc
Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile
939                                                 252
atg acc cag gtg aaa aag aag ccc ttg tgc ctg cag aga gaa gcc aag gtg cct cac ttg cct gcc
Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro Ala
1005                                                274
gat aag gcc cgg ggt aca cag ggc ccc gag cag cag cac ctg ctg atc aca gcg ccg agc tcc agc
Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu Il- Thr Ala Pro Ser Ser Ser
1071                                                296
agc agc tcc ctg gag agc tcg gcc agt gcg ttg gac aga agg gcg ccc act cgg aac cag cca cag
Ser Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln
1137                                                318
gca cca ggc gtg gag gcc agt ggg gcc gcg gag gcc cgg gcc agc acc ggg agc tca gat tct tcc
Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His Gly Thr Gln
1203                                                340
ctt ggt ggc cat ggg acc cag gtc aat gtc acc tgc atc gtg aac gtc tgt agc agc tct gac cac
Ala Pro Gly Val Glu Ala Ser Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser Ser Asp His
1269                                                362
agc tca cag tgc tcc tcc caa gcc agc tcc aca atg gga gac aca gat tcc agc ccc tcg gag tcc
Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser
1335                                                384
ccg aag gac gag cag gtc ccc ttc tcc aag gag gaa tgt gcc ttt cgg tca cag ctg gag acg cca
Pro Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr Pro
1401                                                406
gag acc ctg ctg ggg agc acc gaa gag aag ccc ctg ccc ctt gga gtg cct gat gct ggg atg aag
Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys
1467                                                428
ccc agt taa ccaggccggt gtgggctgtg tcgtagccaa ggtgggctga gccctggcag gatgaccctg cgaaggggc
Pro Ser End
   439
```

TRANSMEMBRANE DOMAIN

FIG. 5C

1545

cctggtcctt ccaggccccc accactagga ctctgaggct ctttctgggc caagttcctc tagtgccctc cacagccgca
gcctccctct gacctgcagg ccaagagcag aggcagcgag ttggggaaag cctctgctgc catggtgtgt ccctctcgga
aggctggctg ggcatggacg ttcggggcat gctggggcaa gtccctgact ctctgtgacc tgccccgccc agctgcacct
gccagcctgg cttctggagc ccttgggttt tttgtttgtt tgtttgtttg tttgtttgtt tctcccccctg ggctctgccc
agctctggct tccagaaaac cccagcatcc ttttctgcag aggggctttc tggagaggag ggatgctgcc tgagtcaccc
atgaagacag gacagtgctt ctgcctgagg cagagactgc gggatggtcc tggggctctg tgtagggagg aggtggcagc
cctgtaggga acggggtcct tcaagttagc tcaggaggct tggaaagcat cacctcaggc caggtgcagt ggctcacgcc
tatgatccca gcactttggg aggctgaggc gggtggatca cctgaggtta ggagttcgag accagcctgg ccaacatggt
aaaaccccat ctctactaaa aatacagaaa ttagccgggc 3683

acctcaggc caggtgcagt ggctcacgcc

2075

FIG. 6

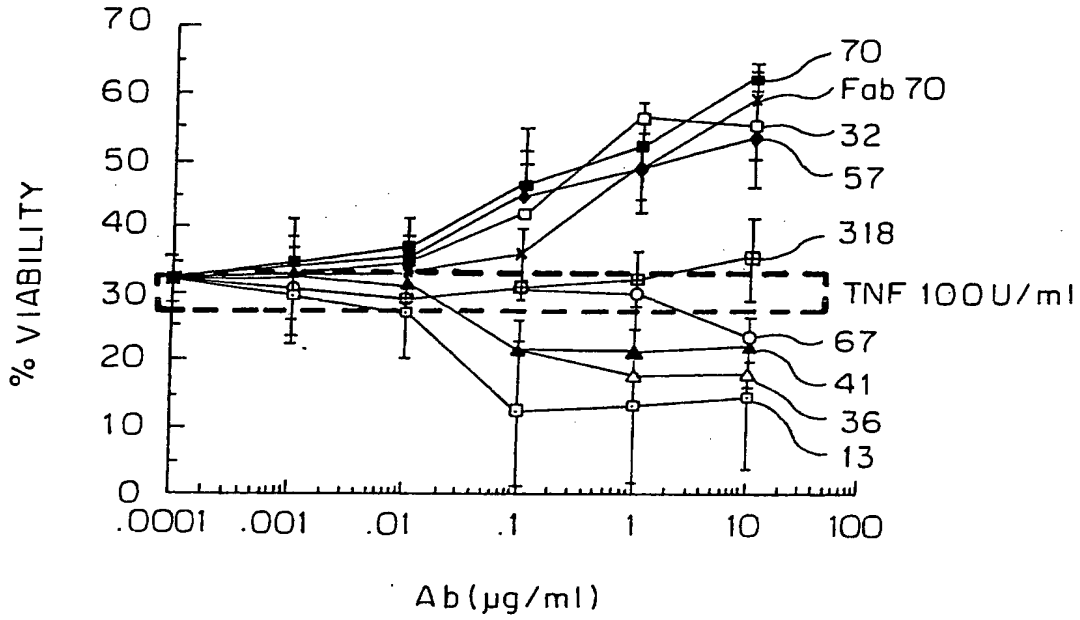

70
60
50
40
30
20
10
0
% VIABILITY
.0001
.001
.01
.1
1
10
100
Ab (μg/ml)
70
Fab 70
32
57
318
TNF 100U/ml
67
41
36
13

FIG. 7

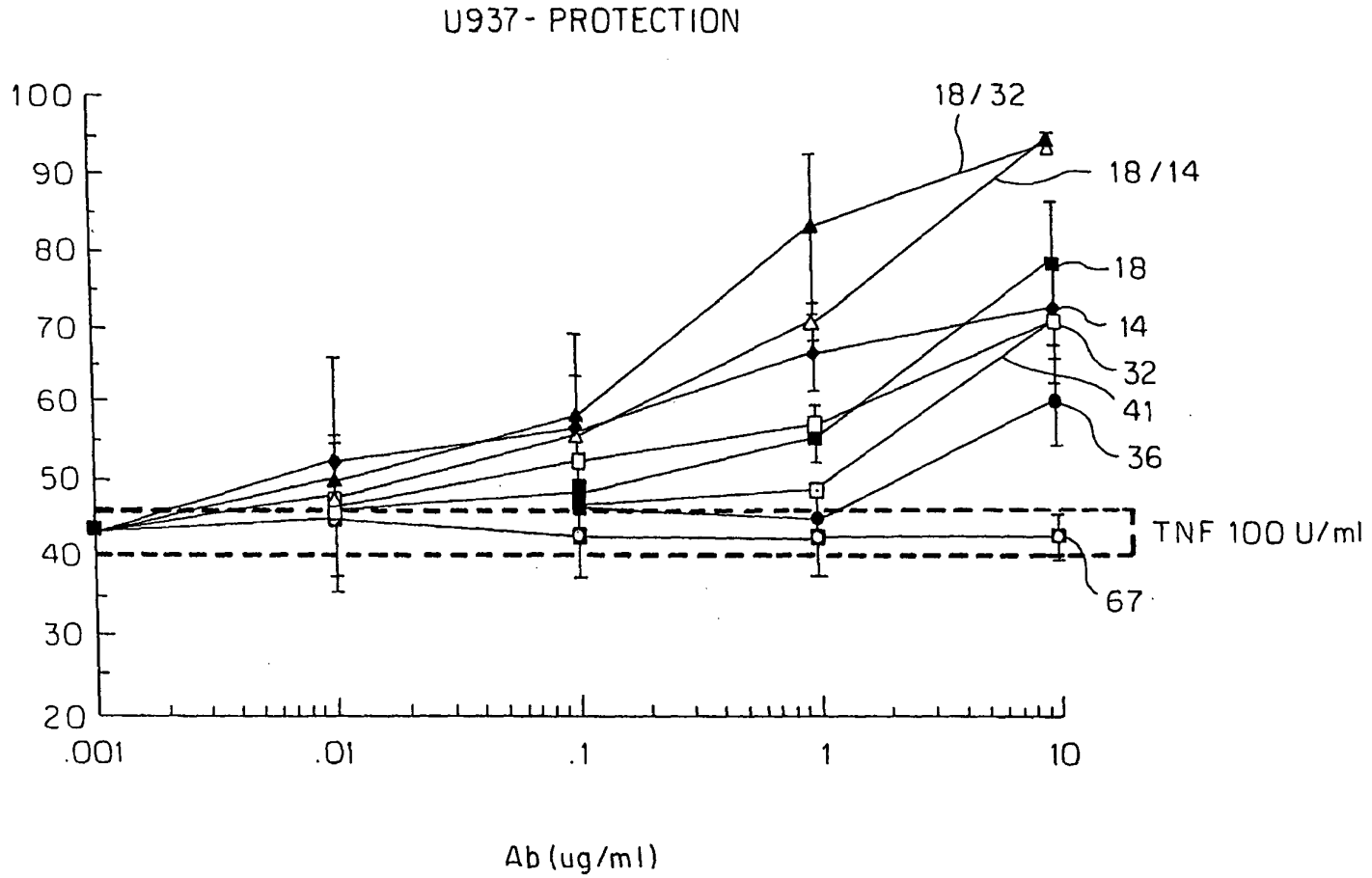

U937 - PROTECTION
100
90
80
70
60
50
40
30
20
.001
.01
.1
1
10
18/32
18/14
18
14
32
41
36
67
TNF 100 U/ml
Ab (ug/ml)

FIG. 8A

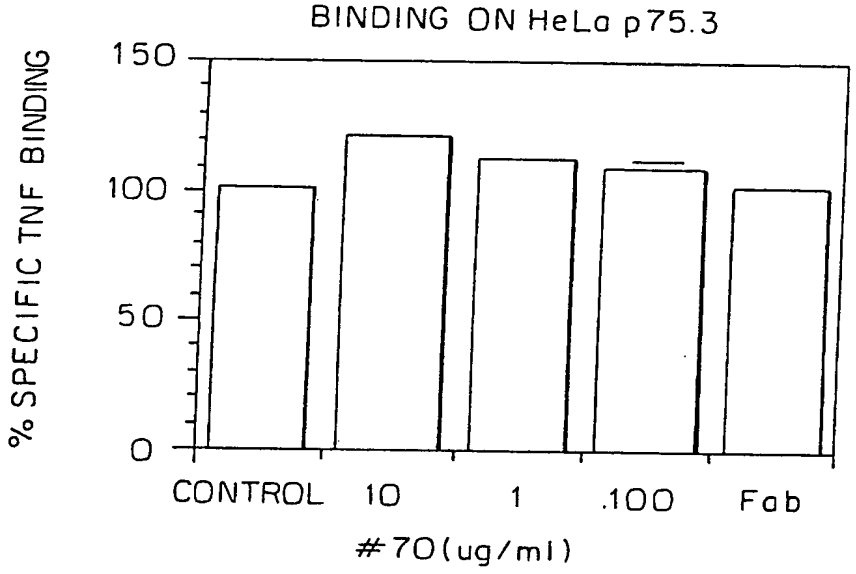

BINDING ON HeLa p75.3
% SPECIFIC TNF BINDING
150
100
50
0
CONTROL
10
1
.100
Fab
#70(ug/ml)

FIG. 8B

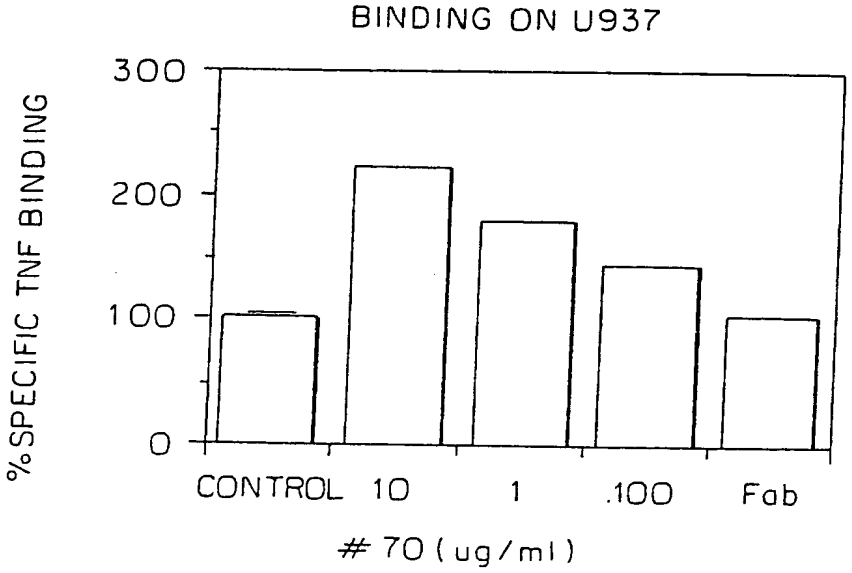

BINDING ON U937
% SPECIFIC TNF BINDING
300
200
100
0
CONTROL
10
1
.100
Fab
70 (ug/ml)

FIG. 9A

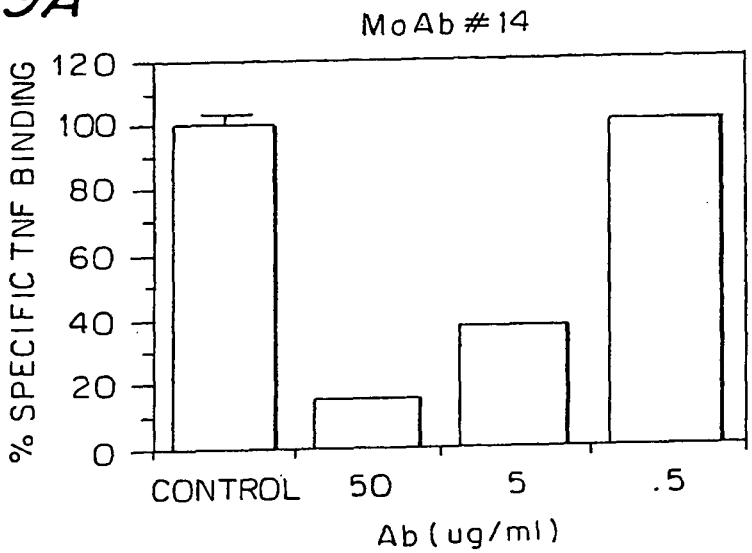


FIG. 9B

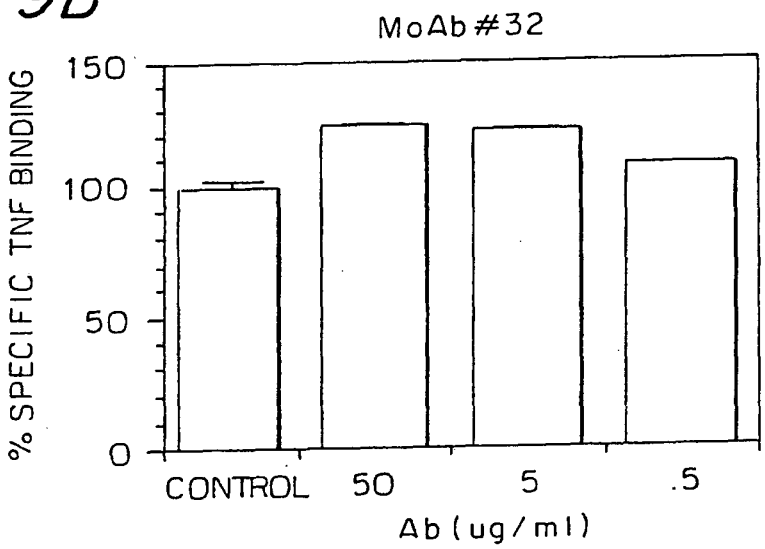


FIG. 9C

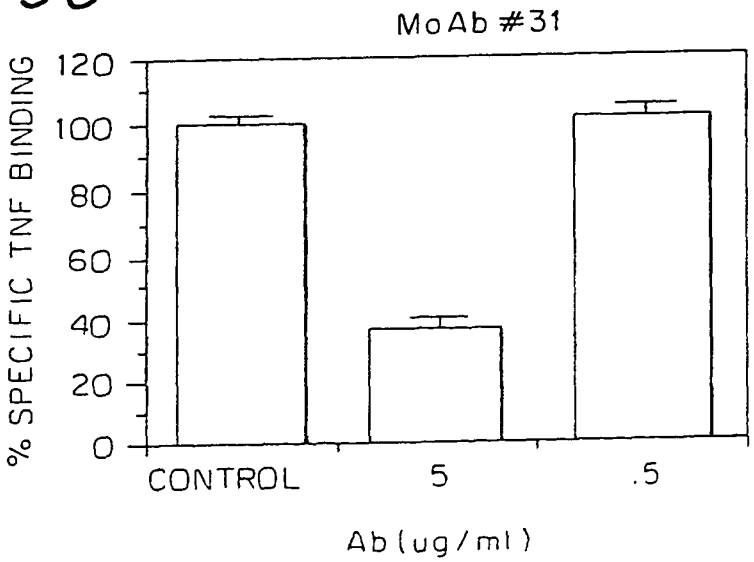


FIG. 9D

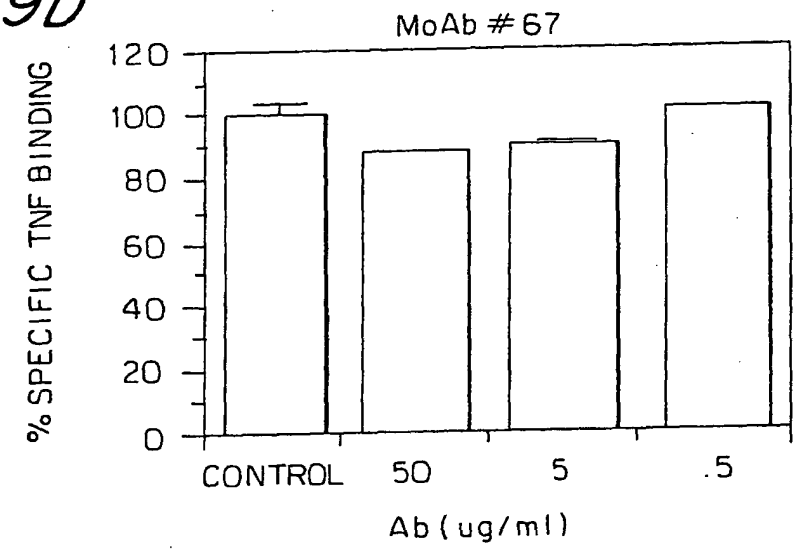


FIG. 9E

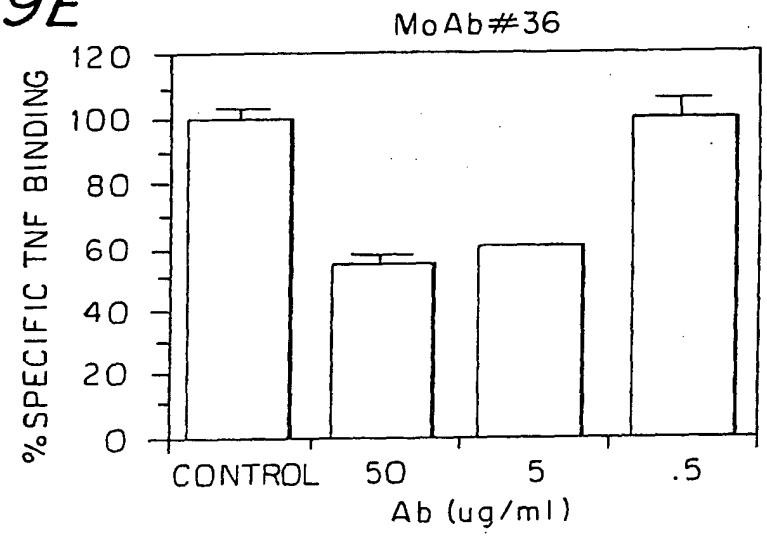


FIG. 9F

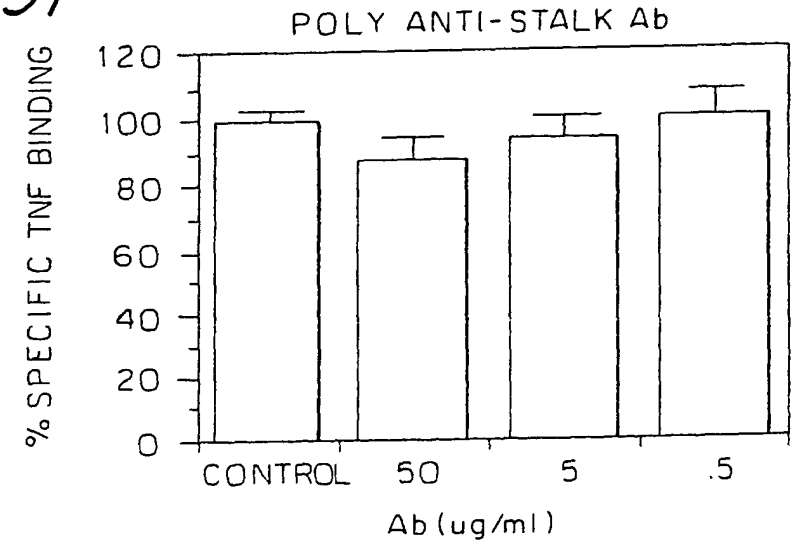


FIG. 10

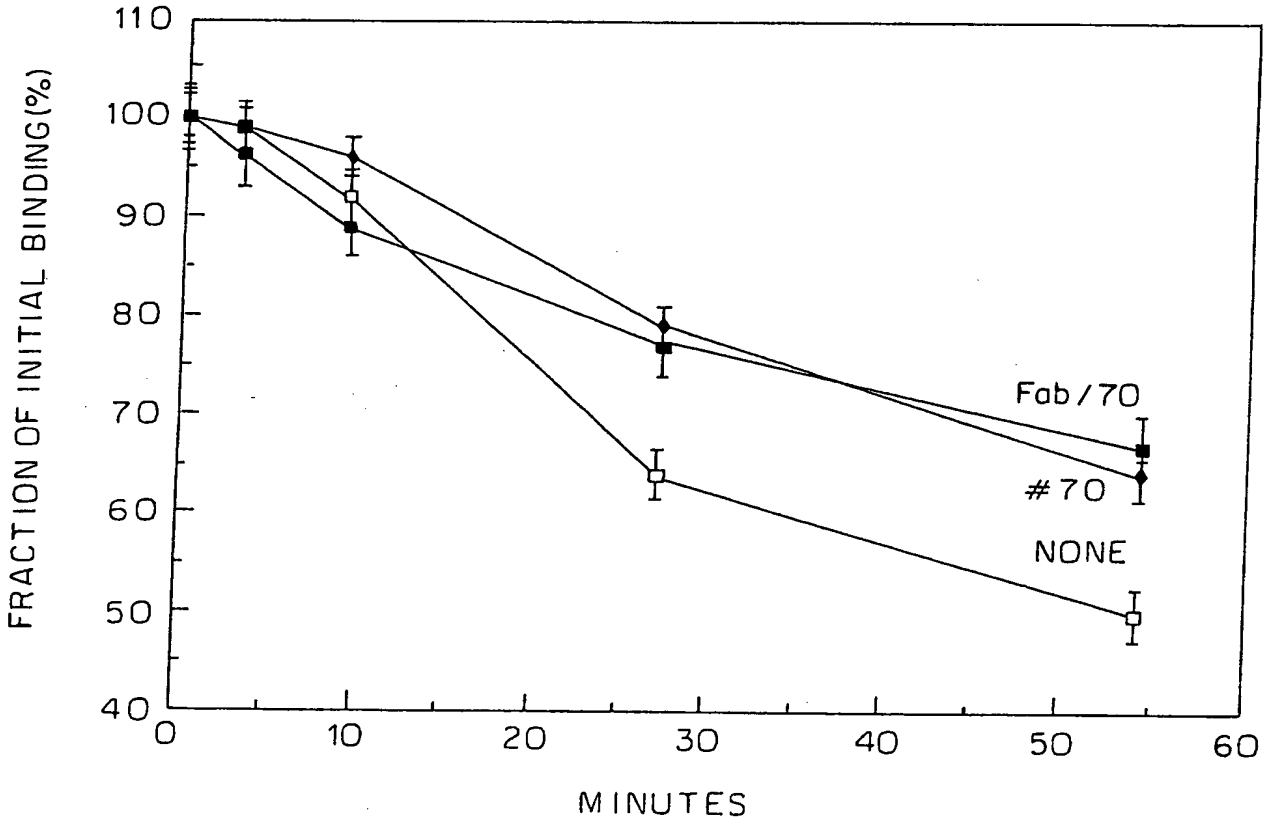

FRACTION OF INITIAL BINDING (%)
110
100
90
80
70
60
50
40
0
10
20
30
40
50
60
MINUTES
Fab / 70
#70
NONE

FIG. 11A

```
     1/1                                                                31/11
#70  GTG AAA CTG CAG GAG TCT GGA CCT GAG CTG GTG AAG CCT GGG GCC TCA GTG AAG ATT TCC
     V   K   L   Q   E   S   G   P   E   L   V   K   P   G   A   S   V   K   I   S
     1/1                                                                31/11
#32                              CCT GAG CTG GTG GCT CCT GGG GCC TCA GTG AAG ATT TCC
                                 P   E   L   V   A   P   G   A   S   V   K   I   S
     1/1                                                                31/11
#57  GTG TCC CTG CAG GAG TCT GGG GGA GGC TTA GTG CAG CCT GGA GGG TCC CGG AAA CTC TCC
     V   S   L   Q   E   S   G   G   G   L   V   Q   P   G   G   S   R   K   L   S

     61/21                                                              91/31
#70  TGC AAA ACT TCT GGC TTC GCA TTC AGT CAT TCT TGG ATG AAC TGG GTG AGG CAG AGG CCT
     C   K   T   S   G   F   A   F   S   H   S   W   M   N   W   V   R   Q   R   P
     61/21                                                              91/31
#32  TGC AAA GCT TCT GGC TAC GCA TTC AGT CAC TCT TGG ATG AAC TGG GTG AAG CAG AGG CCT
     C   K   A   S   G   Y   A   F   S   H   S   W   M   N   W   V   K   Q   R   P
     61/21                                                              91/31
#57  TGT GCA GCT TCT GGA TTC ACT TTC AGT AGC TTT GGA ATG CAC TGG GTT CGT CAG GCT CCA
     C   A   A   S   G   F   T   F   S   S   F   G   M   H   W   V   R   Q   A   P

     121/41                                                             151/51
#70  GGA CAG GGT CTT GAA TGG ATT GGA CGG ATT TAT CCT GGA GAT GGA AAT ACT GAT TAC CCT
     G   Q   G   L   E   W   I   G   R   I   Y   P   G   D   G   N   T   D   Y   N
     121/41                                                             151/51
#32  GGA AAG GGT CTT GAG TGG ATT GGA CGG ATT CAT CCT GGA GAT GGA GAC ACT GAC TAC AAT
     G   K   G   L   E   W   I   G   R   I   H   P   G   D   G   D   T   D   Y   N
     121/41                                                             151/51
#57  GAG AAG GGG CTG GAG TGG GTC GCA TAC ATT AGT AGT GGC AGT AGT ACC CTC CAC TAT GCA
     E   K   G   L   E   W   V   A   Y   I   S   S   G   S   S   T   L   H   Y   A
```

FIG. 11B

```
      181/61                                                  211/71
#70   GGG AAG TTC CAG GGC CAG GCC ACA CTG ACT GCA GAC AAA TCT TCC AGC ACA GCC TAC ATG
      G   K   F   Q   G   Q   A   T   L   T   A   D   K   S   S   S   T   A   Y   M
      181/61                                                  211/71
#32   GGG AAC TTC AGG GGC AAG GCC ACA CTG ACT GCA GAC ACA TCC TCC AGC TCA GCC TAC ATG
      G   N   F   R   G   K   A   T   L   T   A   D   T   S   S   S   S   A   Y   M
      181/61                                                  211/71
#57   GAC ACA GTG AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT CCC AAG AAC ACG CTG TTC CTG
      D   T   V   K   G   R   F   T   I   S   R   D   N   P   K   N   T   L   F   L
```

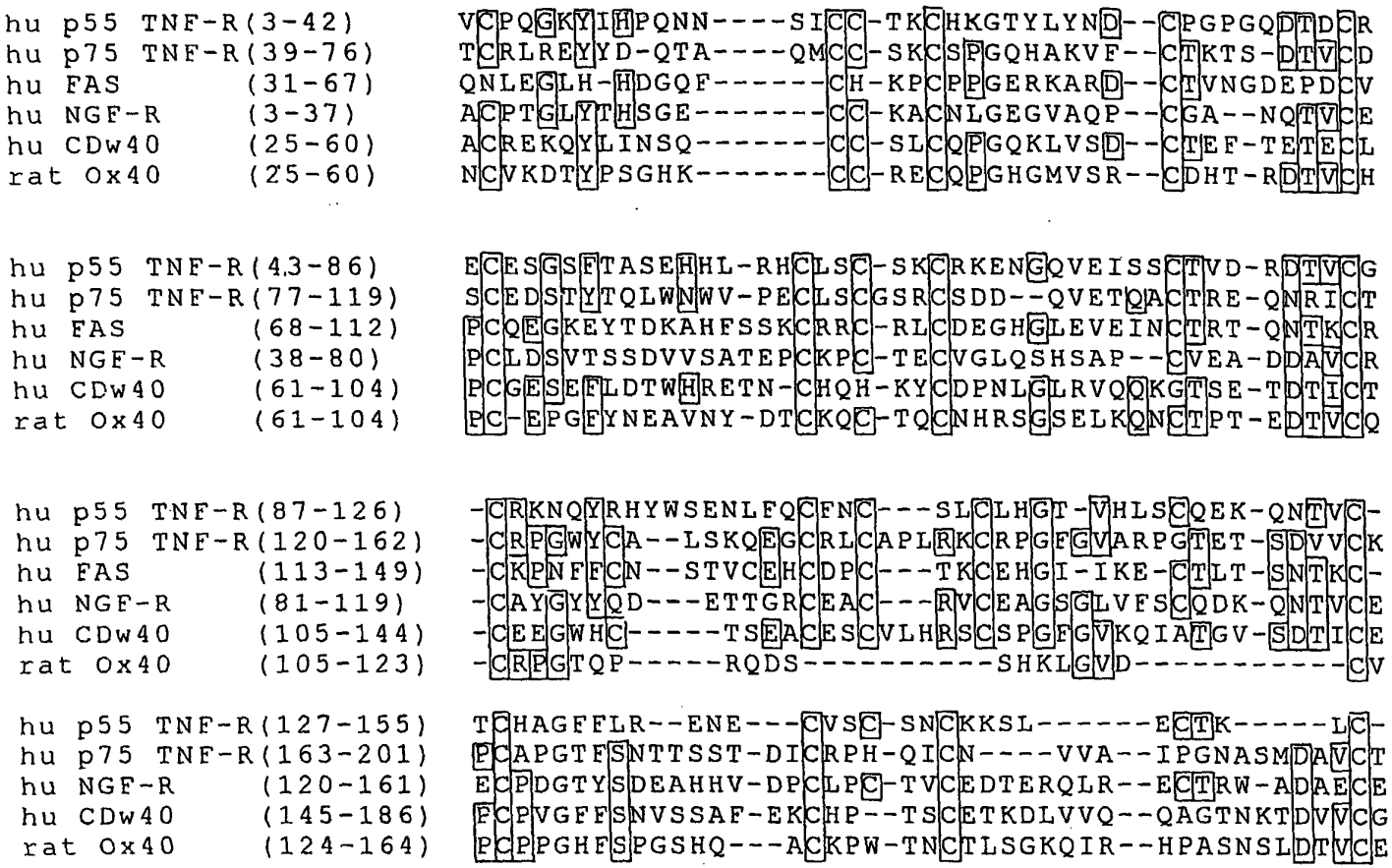
```
      241/81                                                  271/91
#70   CAA CTC TTC AGT CTG ACC TCT GTG GAC TCT GCG GTC TAT TTT TGT GCA CCC GGC CGT TGG
      Q   L   F   S   L   T   S   V   D   S   A   V   Y   F   C   A   P   G   R   W
      241/81
#32   CAG CTC AGC AGC CTG ACC TCT GTG GAT TCT GCG GTC TAC TTC TGT GCA CCC GGC CGT TGG
      Q   L   S   S   L   T   S   V   D   S   A   V   Y   F   C   A   P   G   R   W
      241/81                                                  271/91
#57   CAA ATG AAA CTA CCC TCA CTA TGC TAT GGA CTA CTG GGG CCA AGG GAC CAC GGT CAC CGT
      Q   M   K   L   P   S   L   C   Y   G   L   L   G   P   R   D   H   G   H   R
```

```
      301/101                                                 331/111
#70   TAC CTC GAA GTC TGG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA
      Y   L   E   V   W   G   Q   G   T   T   V   T   V   S   S
      301/101
#32   TAC CTC GAG GTC TGG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA
      Y   L   E   V   W   G   Q   G   T   T   V   T   V   S   S
      301/101
#57   CTC CTC A
      L   L
```

FIG. 12

```
                                                                31/11
                                                TCC TCC CTG GCT ATG TCA GTA GGA CAG ATG GTC ACT
                                                S   S   L   A   M   S   V   G   Q   M   V   T
61/21                                                           91/31
ATG AGC TGC AAG TCC AGT CAG AGC CTT TTA ACT AGT AGC ACT CAA AAG AAC TCT TTG GCC
M   S   C   K   S   S   Q   S   L   L   T   S   S   T   Q   K   N   S   L   A
121/41                                                          151/51
TGG TAC CAG CAG ACA CCA GGA CAG TCT CCT AAA CTT CTG ATA TAC TTT GCA TCC ACT AGG
W   Y   Q   Q   T   P   G   Q   S   P   K   L   L   I   Y   F   A   S   T   R
181/61                                                          211/71
CTA TCT GGG GTC CCT GAT CGC TTC ATA GGC AGT GGA TCT GGG ACA GAT TTC ACT CTT ACC
L   S   G   V   P   D   R   F   I   G   S   G   S   G   T   D   F   T   L   T
241/81                                                          271/91
ATC AGC AGT GTG CAG GCT GAA GAC CTG GCA GAT TAC TTC TGT CAG CAA CAT TAT AGC ACT
I   S   S   V   Q   A   E   D   L   A   D   Y   F   C   Q   Q   H   Y   S   T
301/101                                                         331/111
CCA TTT ACG TTC GGC TCG GGG ACA AAG TTG GAA ATA GAG CGG GCT GAT GCT GCA CCA ACT
P   F   T   F   G   S   G   T   K   L   E   I   E   R   A   D   A   A   P   T
361/121
GTA TCC ATC TTC CCA CCA TCC A
V   S   I   F   P   P   S
```

FIG. 13


hu p55 TNF-R(3-42) VCPQGKYIHPQNN----SICC-TKCHKGTYLYNDC--CPGPGQDTDCR
hu p75 TNF-R(39-76) TCRLREYYD-QTA----QMCC-SKCSPGQHAKVF--CTKTS-DTVCD
hu FAS (31-67) QNLEGLH-HDGQF------CH-KPCPPGERKARD--CTVNGDEPDCV
hu NGF-R (3-37) ACPTGLYTHSGE-------CC-KACNLGEGVAQP--CGA--NQTVCE
hu CDw40 (25-60) ACREKQYLINSQ-------CC-SLCQPGQKLVSD--CTEF-TETECL
rat Ox40 (25-60) NCVKDTYPSGHK-------CC-RECQPGHGMVSR--CDHT-RDTVCH
hu p55 TNF-R(43-86) ECESGSFTASEHHL-RHCLSC-SKCRKENGQVEISSCTVD-RDTVCG
hu p75 TNF-R(77-119) SCEDSTYTQLWNWV-PECLSCGSRCSDD--QVETQACTRE-QNRICT
hu FAS (68-112) PCQEGKEYTDKAHFSSKCRRC-RLCDEGHGLEVEINCTRT-QNTKCR
hu NGF-R (38-80) PCLDSVTSSDVVSATEPCKPC-TECVGLQSHSAP--CVEA-DDAVCR
hu CDw40 (61-104) PCGESEFLDTWHRETN-CHQH-KYCDPNLGLRVQQKGTSE-TDTICT
rat Ox40 (61-104) PC-EPGFYNEAVNY-DTCKQC-TQCNHRSGSELKQNCTPT-EDTVCQ
hu p55 TNF-R(87-126) -CRKNQYRHYWSENLFQCFNC---SLCLHGT-VHLSCQEK-QNTVC-
hu p75 TNF-R(120-162) -CRPGWYCA--LSKQEGCRLCAPLRKCRPGFGVARPGTET-SDVVCK
hu FAS (113-149) -CKPNFFCN--STVCEHCDPC---TKCEHGI-IKE-CTLT-SNTKC-
hu NGF-R (81-119) -CAYGYYQD---ETTGRCEAC---RVCEAGSGLVFSCQDK-QNTVCE
hu CDw40 (105-144) -CEEGWHC-----TSEACESCVLHRSCSPGFGVKQIATGV-SDTICE
rat Ox40 (105-123) -CRPGTQP-----RQDS----------SHKLGVD----------CV
hu p55 TNF-R(127-155) TCHAGFFLR--ENE---CVSC-SNCKKSL------ECTK-----LC-
hu p75 TNF-R(163-201) PCAPGTFSNTTSST-DICRPH-QICN----VVA--IPGNASMDAVCT
hu NGF-R (120-161) ECPDGTYSDEAHHV-DPCLPC-TVCEDTERQLR--ECTRW-ADAECE
hu CDw40 (145-186) FCPVGFFSNVSSAF-EKCHP--TSCETKDLVVQ--QAGTNKTDVVCG
rat Ox40 (124-164) PCPPGHFSPGSHQ---ACKPW-TNCTLSGKQIR--HPASNSLDTVCE